CLAIMS

What is claimed is:

1. An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

2. The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 20: Cys-X_2-X_3-X_4-X_5-X_6-Tyr-Cys (TN8), wherein

X_2 is Ala, Arg, Glu, Lys or Ser;

X_3 is Ala, Asp, Gln, Glu, Thr or Val;

X_4 is Asp or Glu;

X_5 is Trp or Tyr; and

X_6 is Thr or Tyr; or

Loop Consensus Sequence 21: Cys-X_2-X_3-X_4-Gly-X_6-X_7-Cys (TN8), wherein

X_2 is Asp, Gln or His;

X_3 is His or Tyr;

X_4 is His, Ile or Tyr;

X_6 is Ile, Met or Val; and

X_7 is Gly or Tyr; or

Loop Consensus Sequence 22: Cys-X_2-X_3-X_4-X_5-Gly-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;

X_3 is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr or Val;

X_5 is Asp, Phe, Ser, Thr, Trp or Tyr; and

X_7 is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr.

3. The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 23: Cys-X_2-X_3-X_4-X_5-Trp-Gly-Gly-X_9-X_{10}-Cys (SEQ ID NO:3; TN11), wherein

X_2 is Ala, Phe or Trp;

X_3 is Glu or Lys;

X_4 is Asp, Ser, Trp or Tyr;

X_5 is Phe, Pro or Ser;

X_9 is Gln or Glu; and

X_{10} is Ile, Phe or Val; or

Loop Consensus Sequence 24: Cys-X_2-Glu-X_4-Ser-X_6-Ser-X_8-X_9-X_{10}-Phe-Cys (SEQ ID NO:15; TN12), wherein

X_2 is His or Tyr;

X_4 is Leu, His or Thr;

X_6 is Asp or Leu;

X_8 is Gly or Val;

X_9 is Thr or Val; and

X_{10} is Arg or Trp; or

Loop Consensus Sequence 25: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Gly-X_9-Trp-X_{11}-Cys (TN12; SEQ ID NO:16), wherein

X_2 is Glu, Met or Thr;

X_3 is Ile, Leu, Met or Phe;

X_4 is Arg, Asp, Glu, Met, Trp or Val;

X_5 is Asn, Gln, Gly, Ser or Val;

X_6 is Glu or Asp;

X_7 is Lys, Ser, Thr or Val;

X_9 is Arg, Gln, Lys or Trp; and

X_{11} is Asn, Leu, Phe or Tyr; or

Loop Consensus Sequence 26: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Glu or Gly;

X_3 is Trp or Tyr;

X_4 is Ser or Thr;

X_5 is Asn or Gln;

X_6 is Gly or Met;

X_7 is Phe or Tyr;

X_8 is Asp or Gln;

X_9 is Lys or Tyr;

X_{10} is Glu or Thr; and

X_{11} is Glu or Phe.

4. The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 27: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val.

5. The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 28: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Glu, Gly, Lys, Met or Tyr;

X_5 is Ala, Asn, Asp, Leu, Met, Pro or Ser;

X_6 is His, Pro or Trp;

X_7 is His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp.

6. The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:
Loop Consensus Sequence 29: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (SEQ ID NO:1; MTN13), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

7. An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:
Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_16-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or

Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr.

8. The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 6: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-Tyr-Cys-X_{12}-X_{13}-X_{14}, wherein

X_1 is Ala, Arg, Asp, Leu, Lys, Pro, Ser or Val;

X_2 is Asn, Asp, Glu, Lys, Thr or Ser;

X_3 is Ile, Leu, Trp;

X_5 is Ala, Arg, Glu, Lys or Ser;

X_6 is Ala, Asp, Gln, Glu, Thr or Val;

X_7 is Asp or Glu;

X_8 is Trp or Tyr;

X_9 is Thr or Tyr;

X_{12} is Glu, Met, Phe, Trp or Tyr;

X_{13} is Ile, Leu or Met; and

X_{14} is Ile, Leu, Met, Phe or Thr; or

Consensus Sequence 7: Trp-Tyr-Trp-Cys-X_5-X_6-X_7-Gly-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (SEQ ID NO:2), wherein

X_5 is Asp, Gln or His;

X_6 is His or Tyr;

X_7 is Ile, His or Tyr;

X_9 is Ile, Met or Val;

X_{10} is Gly or Tyr;

X_{12} is Asp, Lys or Pro;

X_{13} is Gln, Gly or Trp; and

X_{14} is Phe, Ser or Thr; or

Consensus Sequence 8: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Gly-X_{10}-Cys-X_{12}-X_{13}-X_{14}, wherein

X_1 is Gly, Leu, His, Thr, Trp, Tyr;

X_2 is Ile, Leu, Thr, Trp or Val;

X_3 is Asp, Glu, Gln, Trp or Thr;

X_5 is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;

X_6 is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr or Val;

X_8 is Asp, Phe, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Gln, His, Ile, Lys, Met, Phe, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Glu, His, Met, Pro, Ser or Thr; and

X_{14} is Arg, Gln, Glu, Gly, Phe, Ser, Trp or Tyr.

9. The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 9: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Trp-Gly-Gly-X_{12}-X_{13}-Cys-X_{15}-X_{16}-X_{17} (SEQ ID NO:3), wherein

X_1 is Ser, Phe, Trp, Tyr or Gly;

X_2 is Arg, Gly, Ser or Trp;

X_3 is Ala, Glu, Ile or Val;

X_5 is Ala, Phe or Trp;

X_6 is Glu or Lys;

X_7 is Asp, Ser or Trp;

X_8 is Phe, Pro or Ser;

X_{12} is Gln or Glu;

X_{13} is Ile, Phe or Val;

X_{15} is Gln, Ile, Leu or Phe;

X_{16} is Arg, Gly or Pro; and

X_{17} is Gln, His, Phe, Ser, Tyr or Val; or

Consensus Sequence 10: Tyr-Pro-X_3-Cys-X_5-Glu-X_7-Ser-X_9-Ser-X_{11}-X_{12}-X_{13}-Phe-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:4; TN12), wherein

X_3 is Gly or Trp;

X_5 is His or Tyr;

X_7 is His, Leu or Thr;

X_9 is Asp or Leu;

X_{11} is Gly or Val;

X_{12} is Thr or Val;

X_{13} is Arg or Trp;

X_{16} is Ala or Val;

X_{17} is Asp or Pro; and

X_{18} is Gly or Trp; or

Consensus Sequence 11: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Gly-X_{12}-Trp-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:5; TN12), wherein

X_1 is Asp, Gly, Pro or Ser;

X_2 is Arg, Asn, Asp, Gly or Ser;

X_3 is Gly, Thr, Trp or Tyr;

X_5 is Glu, Met or Thr;

X_6 is Ile, Leu, Met or Phe;

X_7 is Arg, Asp, Glu, Met, Trp or Val;

X_8 is Asn, Gln, Gly, Ser or Val;

X_9 is Asp or Glu;

X_{10} is Lys, Ser, Thr or Val;

X_{12} is Arg, Gln, Lys or Trp;

X_{14} is Asn, Leu, Phe or Tyr;

X_{16} is Gly, Phe, Ser or Tyr;

X_{17} is Gly, Leu, Pro or Ser; and

X_{18} is Ala, Asp, Pro, Ser, Trp or Tyr; or

Consensus Sequence 12: Asn-Trp-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (SEQ ID NO:6; TN12), wherein

X_3 is Glu or Lys;

X_5 is Glu or Gly;

X_6 is Trp or Tyr;

X_7 is Ser or Thr;

X_8 is Asn or Gln;

X_9 is Gly or Met;

X_{10} is Phe or Tyr;

X_{11} is Asp or Gln;

X_{12} is Lys or Tyr;

X_{13} is Glu or Thr;

X_{14} is Glu or Phe;

X_{16} is Ala or Val;

X_{17} is Arg or Tyr; and

X_{18} is Leu or Pro,

wherein the polypeptide binds KDR or a VEGF/KDR complex.

10. An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following: Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr; and

11. The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 187-192, 193-203, and 207-259.

12. The polypeptide of Claim 10, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 137-186.

13. The polypeptide of one of Claims 1, 7 or 10, wherein the polypeptide further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

14. The polypeptide of one of Claims 1, 7 or 10, wherein the polypeptide comprises a modification selected from the group consisting of: an amino acid substitution, and amide bond substitution, a D-amino acid substitution, a glycosylated amino acid, a disulfide bond, a disulfide mimetic substitution, an amino acid translocation, a retroinverso peptide, a peptoid, a retro-inverso peptoid, and a synthetic peptide.

15. The polypeptide of one of Claims 1, 7 or 10, wherein the polypeptide is conjugated to one or more detectable labels or therapeutic agents, optionally further comprising a linker or spacer between the polypeptide and the detectable label or the therapeutic agent.

16. The polypeptide of Claim 15, wherein the detectable label or the therapeutic

agent is selected from the group consisting of: an enzyme, a fluorescent compound, a liposome, an optical dye, one or more paramagnetic metal ions or a superparamagnetic particle, an ultrasound contrast agent and one or more radionuclides.

17. The polypeptide of Claim 16, wherein the therapeutic agent or detectable label comprises one or more radionuclides.

18. The polypeptide of Claim 17, wherein the radionuclide is selected from the group consisting of: ^{18}F, ^{124}I, ^{125}I, ^{131}I, ^{123}I, ^{77}Br, ^{76}Br, ^{99m}Tc, ^{51}Cr, ^{67}Ga, ^{68}Ga, ^{47}Sc, ^{51}Cr, ^{167}Tm, ^{141}Ce, ^{111}In, ^{168}Yb, ^{175}Yb, ^{140}La, ^{90}Y, ^{88}Y, ^{153}Sm, ^{166}Ho, ^{165}Dy, ^{166}Dy, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{97}Ru, ^{103}Ru, ^{186}Re, ^{188}Re, ^{203}Pb, ^{211}Bi, ^{212}Bi, ^{213}Bi, ^{214}Bi, ^{105}Rh, ^{109}Pd, ^{117m}Sn, ^{149}Pm, ^{161}Tb, ^{177}Lu, ^{198}Au and ^{199}Au.

19. The polypeptide of Claim 18, wherein the therapeutic agent or detectable label further comprises a chelator.

20. The polypeptide of Claim 19, wherein the chelator comprises a compound selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.

21. The polypeptide of Claim 19, wherein the radionuclide is ^{99m}Tc or ^{111}In.

22. The polypeptide of Claim 19, wherein the radionuclide is selected from the group consisting of: ^{177}Lu, ^{90}Y, ^{153}Sm and ^{166}Ho.

23. The polypeptide of Claim 16, wherein the detectable label comprises an ultrasound contrast agent.

24. The polypeptide of Claim 23, wherein the ultrasound contrast agent is a phospholipid stabilized microbubble or an ultrasound contrast agent comprising a gas.

25. The polypeptide of Claim 24, wherein the ultrasound contrast agent comprises a fluorinated gas.

26. The polypeptide of Claim 16, wherein the detectable label comprises one or more paramagnetic metal ions and one or more chelators.

27. The polypeptide of Claim 15, wherein the therapeutic agent is selected from the group consisting of: a bioactive agent, a cytotoxic agent, a drug, a chemotherapeutic agent and a radiotherapeutic agent.

28. The polypeptide of Claim 1 or 7, wherein the polypeptide has an apparent K_D for KDR or VEGF/KDR complex of less than 10 μM.

29. The polypeptide of Claim 1 or 7, wherein the polypeptide has an apparent K_D for KDR or VEGF/KDR complex of less than 1.0 μM.

30. The polypeptide of Claim 1 or 7, wherein the polypeptide has an apparent K_D for KDR or VEGF/KDR complex of less than 0.1 μM.

31. The polypeptide of Claim 1 or 7, wherein the polypeptide has an apparent K_D for KDR or VEGF/KDR complex of less than 0.05 μM.

32. A method for isolating phage that bind KDR or a VEGF/KDR complex,

comprising the steps of:

(a) immobilizing a KDR or VEGF/KDR complex target on a solid support;

(b) contacting a library of potential KDR or VEGF/KDR complex binding phage with the solid support to bind KDR or a VEGF/KDR complex binding phage in the library; and

(c) removing the unbound portion of the phage library from the solid support,

thereby isolating phage that bind KDR or a VEGF/KDR complex.

33. A method of detecting KDR or VEGF/KDR complex in an animal or human subject and optionally imaging at least a portion of the animal or human subject comprising the steps of:

(a) detectably labeling a polypeptide of any one of Claims 1, 7 or 10;

(b) administering to the subject the labeled polypeptide; and,

(c) detecting the labeled polypeptide in the subject, and, optionally, constructing an image.

34. The method of Claim 33, wherein the polypeptide is detectably labeled with a label selected from the group consisting of: an enzyme, a fluorescent compound, an ultrasound contrast agent, a liposome and an optical dye, wherein the label optionally further comprises a linker or a spacer.

35. The method of Claim 34, wherein the ultrasound contrast agent is a phospholipid stabilized microbubble or an ultrasound contrast agent comprising a gas.

36. The method of Claim 35, wherein the ultrasound contrast agent comprises a fluorinated gas.

37. The method of Claim 33, wherein the polypeptide is detectably labeled with a label that is one or more radioactive labels, one or more paramagnetic metal atoms or a superparamagnetic particle, and optionally further comprises a linker or a spacer.

38. The method of Claim 37, wherein the radioactive label comprises one or more radionuclides selected from the group consisting of: ^{18}F, ^{124}I, ^{125}I, ^{131}I, ^{123}I, ^{77}Br, ^{76}Br, ^{99m}Tc, ^{51}Cr, ^{67}Ga, ^{68}Ga, ^{47}Sc, ^{51}Cr, ^{167}Tm, ^{141}Ce, ^{111}In, ^{168}Yb, ^{175}Yb, ^{140}La, ^{90}Y, ^{88}Y, ^{153}Sm, ^{166}Ho, ^{165}Dy, ^{166}Dy, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{97}Ru, ^{103}Ru, ^{186}Re, ^{188}Re, ^{203}Pb, ^{211}Bi, ^{212}Bi, ^{213}Bi, ^{214}Bi, ^{105}Rh, ^{109}Pd, ^{117m}Sn, ^{149}Pm, ^{161}Tb, ^{177}Lu, ^{198}Au and ^{199}Au.

39. The method of Claim 38, wherein the radioactive label further comprises at least one chelator.

40. The method of Claim 39, wherein the chelator is selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.

41. The method of Claim 39, wherein the radionuclide is ^{99m}Tc or ^{111}In.

42. The method of Claim 37, wherein the paramagnetic metal atom is selected from the group consisting of: Mn^{2+}, Cu^{2+}, Fe^{2+}, Co^{2+}, Ni^{2+}, Gd^{3+}, Eu^{3+}, Dy^{3+}, Pr^{3+}, Cr^{3+}, Co^{3+}, Fe^{3+}, Ti^{3+}, Tb^{3+}, Nd^{3+}, Sm^{3+}, Ho^{3+}, Er^{3+}, Pa^{4+} and Eu^{2+}.

43. The method of Claim 42, wherein the paramagnetic label further comprises a chelator.

44. The method of Claim 43, wherein the chelator is selected from the group consisting of: DTPA, DO3A, DOTA, EDTA, TETA, EHPG, HBED, NOTA, DOTMA, TETMA, PDTA, TTHA, LICAM, and MECAM.

45. The method of Claim 33, wherein detection of the labeled polypeptide is indicative of the presence of a pathogen selected from the group consisting of: malaria strains, HIV, SIV, simian hemorrhagic fever virus and enterohemorrhagic *E. coli* strains.

46. The method of Claim 33, wherein detection of the labeled polypeptide is indicative of angiogenesis or neovascularization.

47. The method of Claim 36, wherein the ultrasound contrast agent comprises a fluorinated gas selected from the group of: SF_6 freons, CF_4, C_2F_6, C_3F_8, C_4F_{10}, $CBrF_3$, CCl_2F_2, C_2ClF_5, $CBrClF_2$ and perfluorocarbons.

48. The method of Claim 47, wherein the ultrasound contrast agent comprises a perfluorocarbon gas having the formula C_nF_{n+2} wherein n is from 1 to 12.

49. A method of treating a condition involving activation of KDR, comprising administering to an animal or human subject in need of treatment for such a condition a composition comprising at least one polypeptide according to one of Claims 1, 7 or 10.

50. The method of Claim 49, wherein the condition is solid tumor growth.

51. The method of Claim 50, wherein the polypeptide is conjugated with a tumorcidal agent.

52. A method of treating malaria, HIV infection, SIV infection, simian hemorrhagic fever virus infection, and enterohemorrhagic *E. coli* infection comprising administering to an animal or human subject in need of treatment for such condition a composition comprising a polypeptide one of Claims 1, 7 or 10.

53. A recombinant bacteriophage displaying a KDR binding or VEGF/KDR complex binding polypeptide, which polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or

Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13}

(TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr,

and wherein the polypeptide is displayed on the surface of the recombinant bacteriophage.

54. A magnetic resonance imaging contrast agent comprising a KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser,

Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

$X_3$is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr,

wherein the polypeptide is coupled to at least one chelator capable of complexing a paramagnetic metal or at least one superparamagnetic particle, and wherein the polypeptide optionally comprises an N-terminal and/or C-terminal

flanking peptide.

55. A magnetic resonance imaging contrast agent comprising at least one paramagnetic metal atom or superparamagnetic particle and at least one KDR or VEGF/KDR complex binding moiety comprising a polypeptide of one of Claims 1, 7 or 10.

56. The magnetic resonance imaging contrast agent of Claim 55, wherein the magnetic resonance imaging contrast agent further comprises at least one chelator selected from the group consisting of: DTPA, DOTA, EDTA, TETA, EHPG, HBED, NOTA, DOTMA, TETMA, PDTA, TTHA, LICAM and MECAM.

57. The magnetic resonance imaging contrast agent of Claim 56, wherein the chelator is selected from the group consisting of: diethylenetriamine, tetraazacyclododecane and a carboxymethyl-substituted derivative thereof.

58. The magnetic resonance imaging contrast agent of Claim 55, wherein the paramagnetic metal atom is selected from the group consisting of: Mn^{2+}, Cu^{2+}, Fe^{2+}, Co^{2+}, Ni^{2+}, Gd^{3+}, Eu^{3+}, Dy^{3+}, Pr^{3+}, Cr^{3+}, Co^{3+}, Fe^{3+}, Ti^{3+}, Tb^{3+}, Nd^{3+}, Sm^{3+}, Ho^{3+}, Er^{3+}, Pa^{4+} and Eu^{2+}.

59. The magnetic resonance imaging contrast agent of Claim 58, wherein the multivalent cation is Gd^{3+}.

60. A method for identifying KDR or VEGF/KDR complex binding compounds comprising the steps of:

(a) utilizing a KDR or VEGF/KDR complex binding polypeptide of

one of Claims 1, 7 or 10 to form a complex with a KDR or VEGF/KDR complex target;

(b) contacting the complex with one or more potential KDR or VEGF/KDR complex binding compounds; and

(c) determining whether the potential KDR or VEGF/KDR complex binding compound competes with the KDR or VEGF/KDR complex binding polypeptide to form a complex with the KDR or VEGF/KDR complex target.

61. A diagnostic imaging contrast agent comprising a polypeptide of one of Claims 1, 7 or 10.

62. A method of medical imaging comprising administering to an animal or human subject a pharmaceutical preparation of a contrast agent comprising at least one polypeptide of one of Claims 1, 7 or 10, and imaging the contrast agent by a method selected from the group consisting of: magnetic resonance imaging, ultrasound imaging, optical imaging, sonoluminescence imaging, photoacoustic imaging and nuclear imaging.

63. A method of radiotherapy comprising administering to an animal or human subject in need of such therapy a compound comprising at least one polypeptide of one of Claims 1, 7 or 10 conjugated to one or more radionuclides useful for radiotherapy.

64. The method of Claim 63, wherein the compound further comprises one or more chelators.

65. The method of Claim 64, wherein the compound further comprises a spacer or

linker.

66. The method of Claims 64, wherein the chelator is a compound selected from the group consisting of: formula 20, 21, 22, 23, 24 and 25.

67. The method of Claim 63, wherein the radionuclide is ^{186}Re, ^{188}Re, ^{177}Lu, ^{90}Y, ^{153}Sm or ^{166}Ho.

68. A kit for preparation of a radiopharmaceutical comprising a polypeptide of one of Claims 1, 7 or 10, one or more chelators for one or more radionuclides, and one or more reducing agents.

69. A method of targeting genetic material to KDR-expressing cells comprising administering to an animal or a human in need of such genetic material a polypeptide of one of Claims 1, 7 or 10 conjugated to or associated with the genetic material or a delivery vehicle containing such genetic material.

70. A method of screening binding polypeptides identified by phage display for their ability to bind to cells expressing the target comprising the steps of preparing one or more multimeric constructs comprising one or more binding polypeptides; contacting the multimeric constructs with cells expressing the target; and assessing the ability of the multimeric constructs to bind to the target.

71. The method of claim 70, wherein the cells have been engineered by recombinant DNA technology to express the target.

72. The method of Claim 70, wherein the multimeric constructs are detectably labeled.

73. The method of Claim 70, wherein the ability of the multimeric constructs to bind to the target is assessed in the presence of serum.

74. The method of Claim 70, wherein the multimeric constructs comprise biotinylated binding polypeptides complexed with avidin, streptavidin or neutravidin.

75. The method of Claim 70, wherein the target is KDR or the KDR/VEGF complex.

76. A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid selected from the group consisting of:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X10 is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X11 is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X2 is Asn, Asp or Glu;

X3 is Glu, His, Lys or Phe;

X4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X6 is Arg, Gln, Leu, Lys or Val; or

Consensus Sequence IV: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X2 is Ala, Asp, Lys, Ser, Trp or Val;

X3 is Asn, Glu, Gly, His or Leu;

X4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X6 is His, Pro or Trp;

X7 is Ala, Gly, His, Leu, Trp or Tyr; and

X8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

77. A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid sequence selected from:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or

Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr.

78. A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid sequence of one of the following:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X1–X2–X3–Tyr–Trp–Glu–X7–X8–X9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr.

79. The multimeric polypeptide construct of Claim 77, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 187-192, 193-203 and 207-259.

80. The multimeric polypeptide construct of Claim 78, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 137-

186.

81. The multimeric polypeptide construct of any one of Claims 76, 77 or 78, wherein at least one amino acid sequence further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

82. The multimeric polypeptide construct of any of Claims 76, 77 or 78, wherein at least one amino acid sequence comprises a modification selected from the group consisting of: an amino acid substitution, and amide bond substitution, a D-amino acid substitution, a glycosylated amino acid, a disulfide mimetic substitution, an amino acid translocation, a retroinverso peptide, a peptoid, a retro-inverso peptoid, and a synthetic peptide.

83. The multimeric polypeptide construct of any one of Claims 76, 77 or 78, wherein the multimeric polypeptide construct is conjugated to one or more detectable labels or therapeutic agents, optionally further comprising a linker or spacer between the polypeptide and the detectable label or the therapeutic agent.

84. The multimeric polypeptide construct of Claim 83, wherein the detectable label or the therapeutic agent is selected from the group consisting of: an enzyme, a fluorescent compound, a liposome, an optical dye, one or more paramagnetic metal ions or superparamagnetic particles, an ultrasound contrast agent and one or more radionuclides.

85. The multimeric polypeptide construct of Claim 84, wherein the therapeutic agent or detectable label comprises one or more radionuclides.

86. The multimeric polypeptide construct of Claim 85, wherein the radionuclide is selected from the group consisting of: ^{18}F, ^{124}I, ^{125}I, ^{131}I, ^{123}I, ^{77}Br, ^{76}Br, ^{99m}Tc, ^{51}Cr, ^{67}Ga, ^{68}Ga, ^{47}Sc, ^{51}Cr, ^{167}Tm, ^{141}Ce, ^{111}In, ^{168}Yb, ^{175}Yb, ^{140}La, ^{90}Y, ^{88}Y, ^{153}Sm, ^{166}Ho, ^{165}Dy, ^{166}Dy, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{97}Ru, ^{103}Ru, ^{186}Re, ^{188}Re, ^{203}Pb, ^{211}Bi, ^{212}Bi, ^{213}Bi, ^{214}Bi, ^{105}Rh, ^{109}Pd, ^{117}mSn, ^{149}Pm, ^{161}Tb, ^{177}Lu, ^{198}Au and ^{199}Au.

87. The multimeric polypeptide construct of Claim 86, wherein the therapeutic agent or detectable label further comprises a chelator.

88. The multimeric polypeptide construct of Claim 87, wherein the chelator comprises a compound selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.

89. The multimeric polypeptide construct of Claim 87, wherein the radionuclide is ^{99m}Tc or ^{111}In.

90. The multimeric polypeptide construct of Claim 87, wherein the radionuclide is selected from the group consisting of: ^{177}Lu, ^{90}Y, ^{153}Sm and ^{166}Ho.

91. The multimeric polypeptide construct of Claim 84, wherein the detectable label comprises an ultrasound contrast agent.

92. The multimeric polypeptide construct of Claim 91, wherein the ultrasound contrast agent comprises a phospholipid stabilized microbubble or a microballoon comprising a gas.

93. The multimeric polypeptide construct of Claim 91, wherein the ultrasound

contrast agent comprises a fluorinated gas.

94. The multimeric polypeptide construct of Claim 84, wherein the detectable label comprises one or more paramagnetic metal ions and one or more chelators.

95. The multimeric polypeptide construct of Claim 84, wherein the therapeutic agent is selected from the group consisting of: a bioactive agent, a cytotoxic agent, a drug, a chemotherapeutic agent and a radiotherapeutic agent.

96. An ultrasound contrast agent comprising at least one KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following and optionally further comprising N-terminal and/or C-terminal flanking peptides of one or more amino acids:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser,

Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or

Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr,

wherein at least one polypeptide is conjugated to microvesicles filled with gas or material useful for preparing microvesicles filled with gas.

97. The ultrasound contrast agent of Claim 96, wherein the gas filled microvesicles comprise phospholipid stabilized microbubbles or microballoons.

98. The ultrasound contrast agent of Claim 97, wherein the phospholipid stabilized microbubbles or microballoons further comprise a fluorinated gas.

99. A scintigraphic imaging agent comprising at least one KDR or VEGF/KDR

complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr,

wherein at least one polypeptide is coupled to at least one chelator capable of complexing a radionuclide useful for scintigraphic imaging, and wherein the polypeptide optionally further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

100. A scintigraphic imaging agent comprising at least one radionuclide useful in scintigraphic imaging and at least one KDR or VEGF/KDR complex binding moiety comprising a polypeptide of one of Claims 1, 7 or 10.

101. The scintigraphic imaging agent of Claim 100, further comprising at least one chelator selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b and 25.

102. The scintigraphic imaging agent of Claim 101, wherein the radionuclide is selected from the group consisting of ^{99m}Tc and ^{111}In.

103. An agent useful in radiotherapy comprising at least one KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp;

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr;

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent;

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr;

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val,

wherein at least one polypeptide is coupled to at least one chelator capable of complexing a radionuclide useful in radiotherapy and wherein the polypeptide optionally further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

104. An agent useful in radiotherapy comprising at least one radionuclide useful in radiotherapy and at least one KDR or VEGF/KDR complex binding moiety comprising a polypeptide of one of Claims 1, 7 or 10.

105. The agent useful in radiotherapy of Claim 103, further comprising at least one chelator selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b and 25.

106. The agent useful in radiotherapy of Claim 103, wherein the radionuclide is selected from the group consisting of: ^{177}Lu, ^{90}Y, ^{153}Sm and ^{166}Ho.

107. The method of claim 49, wherein the composition further comprises a therapeutic agent.

108. A method of synthesizing a polypeptide or a multimeric polypeptide construct having the ability to bind KDR or VEGF/KDR complex comprising forming a cyclic polypeptide by introducing an amide bond between two side chains.

109. The method of Claim 108, wherein the polypeptide or multimeric polypeptide comprises a linker comprising at least one glycosylated amino acid selected from the group consisting of serine, threonine and homoserine.

110. A method of synthesizing a multimeric polypeptide construct having the ability to bind KDR or VEGF/KDR complex, comprising:

a) treating a first purified peptide monomer with glutaric acid bis-N-hydroxysuccinimidyl ester; and

b) contacting the peptide monomer of (a) with a second purified peptide monomer in the presence of N,N-(Diisopropyl)aminomethylpolystyrene,

thereby forming the multimeric polypeptide, wherein one or both of the purified peptide monomers has the ability to bind KDR or VEGF/KDR complex.

111. A multimeric polypeptide having the ability to bind to KDR or VEGF/KDR complex selected from the group consisting of: D1, D2, D3, D4, D5, D6, D7, D8, D9, D10, D11, D12, D13, D14, D15, D16, D17, D18, D19, D20, D21, D22,

D23, D24, D25, D26, D27, D28 and D29.

112. A dimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR, wherein each peptide of the dimer comprises a sequence selected from the group consisting of:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

Loop Consensus Sequence 16: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X10 is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X11 is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X2 is Asn, Asp or Glu;

X3 is Glu, His, Lys or Phe;

X4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X6 is Arg, Gln, Leu, Lys or Val;

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

113. A dimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR, wherein each peptide of the dimer comprises a sequence selected from the group consisting of:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr;

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr;

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr.

114. A dimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR, wherein each peptide of the dimer comprises a sequence selected from the group consisting of:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X1–X2–X3–Tyr–Trp–Glu–X7–X8–X9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr.

115. The dimeric polypeptide construct of Claim 113, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 187-192, 193-203 and 207-259.

116. The dimeric polypeptide construct of Claim 114, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 137-186.

117. The dimeric polypeptide construct of any one of Claims 112, 113 or 114, wherein at least one amino acid sequence further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

118. The dimeric polypeptide construct of any of Claims 112, 113 or 114, wherein at least one amino acid sequence comprises a modification selected from the group consisting of: an amino acid substitution, and amide bond substitution, a D-amino acid substitution, a disulfide bond, a glycosylated amino acid, a disulfide mimetic substitution, an amino acid translocation, a retroinverso peptide, a peptoid, a retro-inverso peptoid, and a synthetic peptide.

119. The dimeric polypeptide construct of any one of Claims 112, 113 or 114, conjugated to one or more detectable labels or therapeutic agents, optionally further comprising a linker or spacer between the polypeptide and the detectable label or the therapeutic agent.

120. The dimeric polypeptide construct of Claim 119, wherein the detectable label or

the therapeutic agent is selected from the group consisting of: an enzyme, a fluorescent compound, a liposome, an optical dye, one or more paramagnetic metal ions or a superparamagnetic particle, an ultrasound contrast agent and one or more radionuclides.

121. The dimeric polypeptide construct of Claim 120, wherein the therapeutic agent or detectable label comprises one or more radionuclides.

122. The dimeric polypeptide construct of Claim 121, wherein the radionuclide is selected from the group consisting of: ^{18}F, ^{124}I, ^{125}I, ^{131}I, ^{123}I, ^{77}Br, ^{76}Br, ^{99m}Tc, ^{51}Cr, ^{67}Ga, ^{68}Ga, ^{47}Sc, ^{51}Cr, ^{167}Tm, ^{141}Ce, ^{111}In, ^{168}Yb, ^{175}Yb, ^{140}La, ^{90}Y, ^{88}Y, ^{153}Sm, ^{166}Ho, ^{165}Dy, ^{166}Dy, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{97}Ru, ^{103}Ru, ^{186}Re, ^{188}Re, ^{203}Pb, ^{211}Bi, ^{212}Bi, ^{213}Bi, ^{214}Bi, ^{105}Rh, ^{109}Pd, ^{117}mSn, ^{149}Pm, ^{161}Tb, ^{177}Lu, ^{198}Au and ^{199}Au.

123. The dimeric polypeptide construct of Claim 122, wherein the therapeutic agent or detectable label further comprises a chelator.

124. The dimeric polypeptide construct of Claim 123, wherein the chelator comprises a compound selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.

125. The dimeric polypeptide construct of Claim 123, wherein the radionuclide is ^{99m}Tc or ^{111}In.

126. The dimeric polypeptide construct of Claim 123, wherein the radionuclide is selected from the group consisting of: ^{177}Lu, ^{90}Y, ^{153}Sm and ^{166}Ho.

127. The dimeric polypeptide construct of Claim 120, wherein the detectable label comprises an ultrasound contrast agent.

128. The dimeric polypeptide construct of Claim 127, wherein the ultrasound contrast agent comprises a phospholipid stabilized microbubble or a microballoon comprising a gas.

128. The dimeric polypeptide construct of Claim 127, wherein the ultrasound contrast agent comprises a fluorinated gas.

129. The dimeric polypeptide construct of Claim 120, wherein the detectable label comprises one or more paramagnetic metal ions and one or more chelators.

130. The dimeric polypeptide construct of Claim 120, wherein the therapeutic agent is selected from the group consisting of: a bioactive agent, a cytotoxic agent, a drug, a chemotherapeutic agent and a radiotherapeutic agent.

131. The dimeric polypeptide construct of Claims 112, 113 or 114 wherein each peptide of the dimer is selected from an amino acid sequence selected from the group consisting of the sequences listed in Tables 1-11 and 27.

132. A multimeric polypeptide having the ability to bind to KDR or VEGF/KDR complex, wherein the multimeric polypeptide comprises at least one peptide monomer comprising an amino acid sequence selected from the group consisting of those sequences listed in Tables 1-11 and 27.

133. The method of Claims 63 or 103, wherein the agent comprises D13.

134. The method of Claims 60 or 62, wherein the polypeptide is selected from the group consisting of: SEQ ID NOS: 277, 294, 337, 338, 339, 356, 378, 448, 477 and 480.

135. The ultrasound contrast agent of Claim 96, wherein the agent comprises a KDR or KDR/VEGF complex binding moiety selected from the group consisting of: D23 and SEQ ID NOS:294, 338, 356 and 480.

136. The scintigraphic imaging agent of Claim 99, wherein the agent comprises at least one labeled molecules selected from the group consisting of: ^{125}I-D5, ^{111}In-labeled SEQ ID NO:338, ^{111}IN-D4, ^{177}Lu-D11, ^{177}Lu-D13, ^{99m}Tc-labeled SEQ ID NO:339, ^{99m}Tc-labeled SEQ ID NO:277, ^{99m}Tc-labeled SEQ ID NO:378, ^{99m}Tc-D10, ^{99m}Tc-D12 and ^{99m}Tc-D14.

137. A method of inhibiting VEGF-induced vascular permeability comprising administering an agent comprising a peptide of one of Claims 1, 7 or 10.

138. The method of Claim 137, wherein the agent comprises D10.

139. The dimeric polypeptide construct of one of Claims 112, 113 or 114 that has an apparent K_D for KDR or VEGF/KDR complex of less than 10 μM.

140. The dimeric polypeptide construct of Claim 139, wherein the apparent K_D for KDR or VEGF/KDR complex is less than 1 μM.

141. The dimeric polypeptide construct of Claim 139, wherein the apparent K_D for KDR or VEGF/KDR complex is less than 0.1 μM.

142. The dimeric polypeptide construct of Claim 139, wherein the apparent K_D for KDR or VEGF/KDR complex is less than 0.5 μM.

143. The scintigraphic imaging agent of Claim 99, wherein the agent comprises D10.

144. The method of Claim 133, wherein the agent comprises ^{177}Lu-D13.

145. The method of Claim 49, wherein the condition is treated by inhibiting angiogenesis.

146. The method of Claim 110, wherein the multimeric polypeptide is selected from the group consisting of D1, D2, D3, D4, D5, D6, D7, D8, D9, D10, D11, D12, D13, D14, D15, D16, D17, D18, D19, D20, D21, D22, D23, D24, D25, D26, D27, D28 and D29.

147. A recombinant bacteriophage displaying a KDR binding or VEGF/KDR complex binding polypeptide, which polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide,

C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr,

and wherein the polypeptide is displayed on the surface of the recombinant bacteriophage.

148. A recombinant bacteriophage displaying a KDR binding or VEGF/KDR complex binding polypeptide, which polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-

Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val,

and wherein the polypeptide is displayed on the surface of the recombinant bacteriophage.

149. A magnetic resonance imaging contrast agent comprising a KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr,

and wherein the polypeptide is coupled to at least one chelator capable of complexing a paramagnetic metal or at least one paramagnetic particle, and wherein the polypeptide optionally comprises an N-terminal and/or C-terminal flanking peptide.

150. A magnetic resonance imaging contrast agent comprising a KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or

Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val,

and wherein the polypeptide is coupled to at least one chelator capable of complexing a paramagnetic metal or at least one paramagnetic particle, and wherein the polypeptide optionally comprises an N-terminal and/or C-terminal flanking peptide.

151. An ultrasound contrast agent comprising at least one KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following and optionally further comprising N-terminal and/or C-terminal flanking peptides of one or more amino acids:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino

acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr,

and wherein at least one polypeptide is conjugated to microvesicles filled with gas or material useful for preparing microvesicles filled with gas.

152. An ultrasound contrast agent comprising at least one KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following and optionally further comprising N-terminal and/or C-terminal flanking peptides of one or more amino acids:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-

Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val,

and wherein at least one polypeptide is conjugated to microvesicles filled with gas or material useful for preparing microvesicles filled with gas.

153. A scintigraphic imaging agent comprising at least one KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr,

and wherein at least one polypeptide is coupled to at least one chelator capable of complexing a radionuclide useful for scintigraphic imaging, and wherein the polypeptide optionally further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

154. A scintigraphic imaging agent comprising at least one KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or

Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val,

and wherein at least one polypeptide is coupled to at least one chelator capable of complexing a radionuclide useful for scintigraphic imaging, and wherein the polypeptide optionally further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.

155. The multimeric polypeptide construct of Claim 77, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 505-516.

156. The dimeric polypeptide construct of Claim 113, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS:505-516.

157. The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 9A: X_1–X_2–X_3–Cys–X_5–X_6–X_7–X_8–X_9–X_{10}–X_{11}–X_{12}–X_{13}–Cys–X_{15}–X_{16}–X_{17} (TN11; SEQ ID NO:3), wherein

X_1 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Thr, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asp, Asn, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asp, Asn, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_9 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp or Tyr;

X_{10} is Asp, Gln, Glu, Gly, His, Ile, Leu, Phe, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr or Val;

X_{12} is Ala, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{15} is Ala, Asp, Asn, Glu, Gly, Ile, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{16} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{17} is Ala, Arg, Asp, Asn, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr or Val,

wherein the polypeptide binds KDR or VEGF/KDR complex.

158. A method of detecting KDR or VEGF/KDR complex in an animal or human subject and optionally imaging at least a portion of the animal or human subject

comprising the steps of:

(a) detectably labeling a multimeric polypeptide construct of one of Claims 76, 77 or 78;

(b) administering to the subject the labeled multimeric polypeptide construct; and,

(c) detecting the labeled multimeric polypeptide construct in the subject,

and, optionally, constructing an image..

159. The method of Claim 158, wherein the multimeric polypeptide is selected from the group consisting of: D1, D2, D3, D4, D5, D6, D7, D8, D9, D10, D11, D12, D13, D14, D15, D16, D17, D18, D19, D20, D21, D22, D23, D24, D25, D26, D27, D28, and D29.

160. The method of Claim 158, wherein the multimeric polypeptide is detectably labeled with a label selected from the group consisting of: an enzyme, a fluorescent compound, an ultrasound contrast agent, a liposome and an optical dye, wherein the label optionally further comprises a linker a spacer.

161. The method of Claim 160, wherein the ultrasound contrast agent is a phospholipid stabilized microbubble or an ultrasound contrast agent comprising a gas.

162. The method of Claim 161, wherein the ultrasound contrast agent comprises a fluorinated gas.

163. The method of Claim 158, wherein the multimeric polypeptide construct is detectably labeled with a label that is one or more radioactive labels, one or

more paramagnetic metal atoms or a superparamagnetic particle, and optionally further comprises a linker or a spacer.

164. The method of Claim 163, wherein the radioactive label comprises one or more radionuclides selected from the group consisting of: ^{18}F, ^{124}I, ^{125}I, ^{131}I, ^{123}I, ^{77}Br, ^{76}Br, ^{99m}Tc, ^{51}Cr, ^{67}Ga, ^{68}Ga, ^{47}Sc, ^{51}Cr, ^{167}Tm, ^{141}Ce, ^{111}In, ^{168}Yb, ^{175}Yb, ^{140}La, ^{90}Y, ^{88}Y, ^{153}Sm, ^{166}Ho, ^{165}Dy, ^{166}Dy, ^{62}Cu, ^{64}Cu, ^{67}Cu, ^{97}Ru, ^{103}Ru, ^{186}Re, ^{188}Re, ^{203}Pb, ^{211}Bi, ^{212}Bi, ^{213}Bi, ^{214}Bi, ^{105}Rh, ^{109}Pd, ^{117m}Sn, ^{149}Pm, ^{161}Tb, ^{177}Lu, ^{198}Au and ^{199}Au.

165. The method of Claim 164, wherein the radioactive label further comprises at least one chelator.

166. The method of Claim 165, wherein the chelator is selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.

167. The method of Claim 165, wherein the radionuclide is ^{99m}Tc or ^{111}In.

168. The method of Claim 163, wherein the paramagnetic metal atom is selected from the group consisting of: Mn^{2+}, Cu^{2+}, Fe^{2+}, Co^{2+}, Ni^{2+}, Gd^{3+}, Eu^{3+}, Dy^{3+}, Pr^{3+}, Cr^{3+}, Co^{3+}, Fe^{3+}, Ti^{3+}, Tb^{3+}, Nd^{3+}, Sm^{3+}, Ho^{3+}, Er^{3+}, Pa^{4+} and Eu^{2+}.

169. The method of Claim 168, wherein the paramagnetic label further comprises a chelator.

170. The method of Claim 169, wherein the chelator is selected from the group consisting of: DTPA, DO3A, DOTA, EDTA, TETA, EHPG, HBED, NOTA, DOTMA, TETMA, PDTA, TTHA, LICAM, and MECAM.

171. The method of Claim 158, wherein detection of the labeled multimeric polypeptide construct is indicative of the presence of a pathogen selected from the group consisting of: malaria strains, HIV, SIV, simian hemorrhagic fever virus and enterohemorrhagic *E. coli* strains.

172. The method of Claim 158, wherein detection of the labeled multimeric polypeptide construct is indicative of angiogenesis or neovascularization.

173. The method of Claim 162, wherein the ultrasound contrast agent comprises a fluorinated gas selected from the group of: SF_6 freons, CF_4, C_2F_6, C_3F_8, C_4F_{10}, $CBrF_3$, CCI_2F_2, C_2ClF_5, $CBrClF_2$ and perfluorocarbons.

174. The method of Claim 173, wherein the ultrasound contrast agent comprises a perfluorocarbon gas having the formula C_nF_{n+2} wherein n is from 1 to 12.

175. A multimeric polypeptide having the ability to bind to KDR or VEGF/KDR complex selected from the group consisting of: D30 and D31.

176. The scintigraphic imaging agent of Claim 99, wherein the agent comprises ^{99m}Tc-D30.

177. The method of Claim 110, wherein the multimeric polypeptide construct is selected from the group consisting of: D30 and D31.

178. The method of Claim 158, wherein the multimeric polypeptide construct is selected from the group consisting of: D30 and D31.

179. A method of treating a condition involving activation of KDR, comprising administering to an animal or human subject in need of treatment for such a condition a composition comprising at least one multimeric polypeptide construct according to one of Claims 76, 77 or 78.

180. The method of Claim 179, wherein the condition is solid tumor growth.

181. The method of Claim 50, wherein the polypeptide construct is conjugated with a tumorcidal agent.

182. A method of medical imaging comprising administering to an animal or human subject a pharmaceutical preparation of a contrast agent comprising at least one multimeric polypeptide construct of one of Claims 76, 77 or 78, and imaging the contrast agent by a method selected from the group consisting of: magnetic resonance imaging, ultrasound imaging, optical imaging, sonoluminescence imaging, photoacoustic imaging and nuclear imaging.

183. A method of radiotherapy comprising administering to an animal or human subject in need of such therapy a compound comprising at least one multimeric polypeptide construct of one of Claims 76, 77 or 78 conjugated to one or more radionuclides useful for radiotherapy.

184. The method of Claim 183, wherein the compound further comprises one or more chelators.

185. The method of Claim 184, wherein the multimeric polypeptide further comprises a spacer or linker.

186. The method of Claims 184, wherein the chelator is a compound selected from the group consisting of: formula 20, 21, 22, 23, 24 and 25.

187. The method of Claim 183, wherein the radionuclide is ^{186}Re, ^{188}Re, ^{177}Lu, ^{90}Y, ^{153}Sm or ^{166}Ho.

188. A method of targeting genetic material to KDR-expressing cells comprising administering to an animal or a human in need of such genetic material a multimeric polypeptide construct of one of Claims 76, 77 or 78 conjugated to or associated with the genetic material or a delivery vehicle containing such genetic material.

189. The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence selected form the group consisting of SEQ ID NOS: 505-616.

190. The multimeric polypeptide construct of Claim 77, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 505-616.

191. The dimeric polypeptide construct of Claim 113, comprising at least one amino acid sequence selected from the group consisting of: SEQ ID NOS: 505-616.

192. A method of inhibiting angiogenesis comprising administering to an animal or human subject in need of treatment for such condition a polypeptide having the ability to bind to KDR or VEGF/KDR complex, or a multimeric polypeptide construct comprising at least one polypeptide having the ability to bind to KDR or VEGF/KDR complex, the polypeptide comprising an amino

acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp;

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr;

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent;

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr;

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser,

Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

193. The method according to Claim 192, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 137-186, 187-192, 193-203, and 207-259.

194. The method according to Claim 192, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 505-616.

195. A method of inhibiting VEGF activation of KDR comprising administering to

an animal or human subject in need of treatment for such condition a polypeptide having the ability to bind to KDR or VEGF/KDR complex, or a multimeric polypeptide construct comprising at least one ploypeptide having the ability to bind to KDR or VEGF/KDR complex, sadi polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14} (TN8), wherein

X_1 is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X_2 is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X_3 is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X_5 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_6 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_7 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_9 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X_{10} is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X_{12} is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X_{14} is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18} (TN12), wherein

X_1 is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X_2 is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_5 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_6 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_7 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_9 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_{10} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_{11} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_{12} is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{13} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X_{14} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X_{16} is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{17} is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X_{18} is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X_1-X_2-X_3-Cys-X_5-X_6-X_7-Gly-X_9-Cys-X_{11}-X_{12}-X_{13} (TN7), wherein

X_1 is Gly or Trp;

X_2 is Ile, Tyr or Val;

X_3 is Gln, Glu, Thr or Trp;

X_5 is Asn, Asp or Glu;

X_6 is Glu, His, Lys or Phe;

X_7 is Asp, Gln, Leu, Lys, Met or Tyr;

X_9 is Arg, Gln, Leu, Lys or Val;

X_{11} is Arg, Phe, Ser, Trp or Val;

X_{12} is Glu, His or Ser; and

X_{13} is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15} (TN9), wherein

X_1 is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X_2 is Asp, Gly, His, Pro or Trp;

X_3 is Gly, Pro, Phe, Thr or Trp;

X_5 is Ala, Asp, Lys, Ser, Trp or Val;

X_6 is Asn, Glu, Gly, His or Leu;

X_7 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_8 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_9 is His, Pro or Trp;

X_{10} is Ala, Gly, His, Leu, Trp or Tyr;

X_{11} is Ala, Asp, Gln, Leu, Met, Thr or Trp;

X_{13} is Ala, Lys, Ser, Trp or Tyr;

X_{14} is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and

X_{15} is Asn, Gln, Glu, Leu, Met, Pro or Trp;

Consensus Sequence 5: X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-Ser-Gly-Pro-X_{12}-X_{13}-X_{14}-X_{15}-Cys-X_{17}-X_{18}-X_{19} (SEQ ID NO:1; MTN13), wherein

X_1 is Arg, Glu, His, Ser or Trp;

X_2 is Asn, Asp, Leu, Phe, Thr or Val;

X_3 is Arg, Asp, Glu, His, Lys or Thr;

X_5 is Asp, Glu, His or Thr;

X_6 is Arg, His, Lys or Phe;

X_7 is Gln, Ile, Lys, Tyr or Val;

X_8 is Gln, Ile, Leu, Met or Phe;

X_{12} is Asn, Asp, Gly, His or Tyr;

X_{13} is Gln, Gly, Ser or Thr;

X_{14} is Glu, Lys, Phe or Ser;

X_{15} is Glu, Ile, Ser or Val;

X_{17} is Glu, Gly, Lys, Phe, Ser or Val;

X_{18} is Arg, Asn, Ser or Tyr; and

X_{19} is Asp, Gln, Glu, Gly, Met or Tyr;

Consensus Sequence 13: Z_1-X_1-X_2-X_3-X_4-X_5-Z_2 (Lin20); wherein,

Z_1 is a polypeptide of at least one amino acid or is absent;

X_1 is Ala, Asp, Gln or Glu;

X_2 is Ala, Asp, Gln, Glu, Pro;

X_3 is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X_4 is Asp, Leu, Ser, Trp, Tyr or Val;

X_5 is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z_2 is a polypeptide of at least one amino acid or is absent;

Consensus Sequence 14: X_1–X_2–X_3–Tyr–Trp–Glu–X_7–X_8–X_9–Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X_1 is Asp, Gly or Ser;

X_2 is Ile, Phe or Tyr;

X_3 is Ala, Ser or Val;

X_7 is Gln, Glu, Ile or Val;

X_8 is Ala, Ile or Val;

X_9 is Ala, Glu, Val or Thr;

Loop Consensus Sequence 15: Cys-X_2-X_3-X_4-X_5-X_6-X_7-Cys (TN8), wherein

X_2 is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_4 is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);

X_5 is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X_6 is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and

X_7 is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys (TN12), wherein

X_2 is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X_3 is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X_4 is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X_5 is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X_6 is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X_7 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X_8 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X_9 is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X_{10} is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and

X_{11} is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X_2-X_3-X_4-Gly-X_6-Cys (TN7), wherein

X_2 is Asn, Asp or Glu;

X_3 is Glu, His, Lys or Phe;

X_4 is Asp, Gln, Leu, Lys, Met or Tyr; and

X_6 is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X_2-X_3-X_4-X_5-X_6-X_7-X_8-Cys (TN9), wherein

X_2 is Ala, Asp, Lys, Ser, Trp or Val;

X_3 is Asn, Glu, Gly, His or Leu;

X_4 is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X_5 is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X_6 is His, Pro or Trp;

X_7 is Ala, Gly, His, Leu, Trp or Tyr; and

X_8 is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X_2-X_3-X_4-X_5-Ser-Gly-Pro-X_9-X_{10}-X_{11}-X_{12}-Cys (MTN13; SEQ ID NO:1), wherein

X_2 is Asp, Glu, His or Thr;

X_3 is Arg, His, Lys or Phe;

X_4 is Gln, Ile, Lys, Tyr or Val;

X_5 is Gln, Ile, Leu, Met or Phe;

X_9 is Asn, Asp, Gly, His or Tyr;

X_{10} is Gln, Gly, Ser or Thr;

X_{11} is Glu, Lys, Phe or Ser; and

X_{12} is Glu, Ile, Ser or Val.

196. The method according to Claim 195, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 137-186, 187-192, 193-203, and 207-259.

197. The method according to Claim 195, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 505-616.

198. The method according to Claim 195, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 140, 267, 269, 294, 301, 305, 306, 307, 366, and 277.